DISTRIBUTION OF HLA-DPB1 ALLELES AND TCE GROUPS IN GROUPS OF PATIENTS WITH ACUTE MYELOID LEUKEMIA AND POTENTIAL STEM CELL DONORS IN SERBIA

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HLA-DPB1 belongs to HLA class II and, alongside with HLA-DRB1, represents a highly polymorphic locus whose importance is reflected in hematopoietic stem cell transplantation (HSCT), particularly in the context of allelic mismatching. The T-cell epitope (TCE) model was created in order to more accurately assess the immunogenicity of HLA-DPB1 mismatches. It was predicted that each group would have a distinct level of immunogenic potential, with TCE1 high, TCE2 intermediate, and TCE3 low. TCE classification of HLA-DPB1 allele facilitates ideal donor selection. This study aimed to look into the population's TCE groups and HLA-DPB1 genotypic and allelic distributions. A retrospective analysis included group of 177 patients with AML and 1445 Serbian donors. DNA samples were isolated using automated methods Maxwell-16 (Promega USA) and SaMag-12 (Sacace, Como, Italy). HLA typing was performed by PCR-SSO (One Lambda, USA), PCR-SSP (Olerup, Sweden), NGS (GenDx, The Netherlands) and sequencing on Illumina NovaSeq6000 (Dresden, Germany). HLA-DPB1*04:01 was the most frequent allele in both groups – Serbian donors (38,89%) and patients (36,16%). The HLA-DPB1*02:01, *04:01 genotype was more prevalent in healthy donors (15.08% vs. 9.60%; OR = 0.59, 95% CI: 0.35–1.00; p=0.05). TCE groups 3/3 was equally frequent in the group of patients as were in a group of Serbian donors (71,76% vs 71,18%). While no statistically significant differences were found in the TCE groups, the results suggest possible genotypic variations in HLA-DPB1 alleles. These observed data, for the first time in our population, can help us better understand the possible immunological impact of HSCT in the Serbian population.

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